

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/519,336

Source: PG

Date Processed by STIC: 1/26/06

ENTERED



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/519,336

DATE: 01/26/2006

TIME: 09:07:01

Input Set : F:\G-194US04PCT-Subst-Seq-List.txt

Output Set: N:\CRF4\01262006\J519336.raw

3 <110> APPLICANT: Daniel Cohen,
 4 Ilya Chumakov,
 5 Marta Blumenfeld,
 6 Sanober Shaikh,
 7 Marta Palicio-Barron,
 8 Hadi Abderrahim,
 9 Pascale Grel

11 <120> TITLE OF INVENTION: USE OF PP2A PHOSPHATASE MODULATORS IN THE TREATMENT OF
 MENTAL DISORDERS

13 <130> FILE REFERENCE: G-194US04PCT
 15 <140> CURRENT APPLICATION NUMBER: US 10/519,336
 16 <141> CURRENT FILING DATE: 2004-12-22
 18 <150> PRIOR APPLICATION NUMBER: US 60/391,359
 19 <151> PRIOR FILING DATE: 2002-06-25
 21 <160> NUMBER OF SEQ ID NOS: 47
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1932
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(1932)
 34 <400> SEQUENCE: 1

35 atg gtg cag aag tcg cgc aac ggc ggc gta tac ccc ggc ccg agc ggg 48
 36 Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
 37 1 5 10 15
 39 gag aag aag ctg aag gtg ggc ttc gtg ggg ctg gac ccc ggc gcg ccc 96
 40 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
 41 20 25 30
 43 gac tcc acc cgg gac ggg gcg ctg atc gcc ggc tcc gag gcc ccc 144
 44 Asp Ser Thr Arg Asp Gly Ala Leu Ile Ala Gly Ser Glu Ala Pro
 45 35 40 45
 47 aag cgc ggc agc atc ctc agc aaa cct cgc gcg ggc ggc gcg ggc gcc 192
 48 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
 49 50 55 60
 51 ggg aag ccc ccc aag cgc aac gcc ttc tac cgc aag ctg cag aat ttc 240
 52 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
 53 65 70 75 80
 55 ctc tac aac gtg ctg gag cgg ccg cgc ggc tgg gcg ttc atc tac cac 288
 56 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
 57 85 90 95
 59 gcc tac gtg ttc ctc ctg gtt ttc tcc tgc ctc gtg ctg tct gtg ttt 336
 60 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe

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61	100	105	110	
63 tcc acc atc aag gag tat gag aag agc tcg gag ggg gcc ctc tac atc				384
64 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile				
65	115	120	125	
67 ctg gaa atc gtg act atc gtg gtg ttt ggc gtg gag tac ttc gtg cgg				432
68 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg				
69	130	135	140	
71 atc tgg gcc gca ggc tgc tgc tgc cgg tac cgt ggc tgg agg ggg cgg				480
72 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg				
73 145	150	155	160	
75 ctc aag ttt gcc cgg aaa ccg ttc tgt gtg att gac atc atg gtg ctc				528
76 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu				
77	165	170	175	
79 atc gcc tcc att gcg gtg ctg gcc gcc ggc tcc cag ggc aac gtc ttt				576
80 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe				
81	180	185	190	
83 gcc aca tct gcg ctc cgg agc ctg cgc ttc ctg cag att ctg cgg atg				624
84 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met				
85	195	200	205	
87 atc cgc atg gac cgg cgg gga ggc acc tgg aag ctg ctg ggc tct gtg				672
88 Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val				
89	210	215	220	
91 gtc tat gcc cac agc aag gag ctg gtc act gcc tgg tac atc ggc ttc				720
92 Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe				
93 225	230	235	240	
95 ctt tgt ctc atc ctg gcc tcg ttc ctg gtg tac ttg gca gag aag ggg				768
96 Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly				
97	245	250	255	
99 gag aac gac cac ttt gac acc tac gcg gat gca ctc tgg tgg ggc ctg				816
100 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu				
101	260	265	270	
103 atc acg ctg acc acc att ggc tac ggg gac aag tac ccc cag acc tgg				864
104 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp				
105	275	280	285	
107 aac ggc agg ctc ctt gcg gca acc ttc acc ctc atc ggt gtc tcc ttc				912
108 Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe				
109	290	295	300	
111 ttc gcg ctg cct gca ggc atc ttg ggg tct ggg ttt gcc ctg aag gtt				960
112 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val				
113 305	310	315	320	
115 cag gag cag cac agg cag aag cac ttt gag aag agg cgg aac ccg gca				1008
116 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala				
117	325	330	335	
119 gca ggc ctg atc cag tcg gcc tgg aga ttc tac gcc acc aac ctc tcg				1056
120 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser				
121	340	345	350	
123 cgc aca gac ctg cac tcc acg tgg cag tac tac gag cga acg gtc acc				1104
124 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr				
125	355	360	365	

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127	gtg	ccc	atg	tac	agt	tcg	caa	act	caa	acc	tac	ggg	gcc	tcc	aga	ctt	1152
128	Val	Pro	Met	Tyr	Ser	Ser	Gln	Thr	Gln	Thr	Tyr	Gly	Ala	Ser	Arg	Leu	
129		370					375					380					
131	atc	ccc	ccg	ctg	aac	cag	ctg	gag	ctg	ctg	agg	aac	ctc	aag	agt	aaa	1200
132	Ile	Pro	Pro	Leu	Asn	Gln	Leu	Glu	Leu	Leu	Arg	Asn	Leu	Lys	Ser	Lys	
133	385					390					395					400	
135	tct	gga	ctc	gct	ttc	agg	aag	gac	ccc	ccg	ccg	gag	ccg	tct	cca	agt	1248
136	Ser	Gly	Leu	Ala	Phe	Arg	Lys	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Ser	
137					405					410					415		
139	aaa	ggc	agc	ccg	tgc	aga	ggg	ccc	ctg	tgt	gga	tgc	tgc	ccc	gga	cgc	1296
140	Lys	Gly	Ser	Pro	Cys	Arg	Gly	Pro	Leu	Cys	Gly	Cys	Cys	Pro	Gly	Arg	
141				420					425					430			
143	tct	agc	cag	aag	gtc	agt	ttg	aaa	gat	cgt	gtc	ttc	tcc	agc	ccc	cga	1344
144	Ser	Ser	Gln	Lys	Val	Ser	Leu	Lys	Asp	Arg	Val	Phe	Ser	Ser	Pro	Arg	
145			435					440						445			
147	ggc	gtg	gct	gcc	aag	ggg	aag	ggg	tcc	ccg	cag	gcc	cag	act	gtg	agg	1392
148	Gly	Val	Ala	Ala	Lys	Gly	Lys	Gly	Ser	Pro	Gln	Ala	Gln	Thr	Val	Arg	
149		450					455					460					
151	cgg	tca	ccc	agc	gcc	gac	cag	agc	ctc	gag	gac	agc	ccc	agc	aag	gtg	1440
152	Arg	Ser	Pro	Ser	Ala	Asp	Gln	Ser	Leu	Glu	Asp	Ser	Pro	Ser	Lys	Val	
153	465					470					475					480	
155	ccc	aag	agc	tgg	agc	ttc	ggg	gac	cgc	agc	cgg	gca	cgc	cag	gct	ttc	1488
156	Pro	Lys	Ser	Trp	Ser	Phe	Gly	Asp	Arg	Ser	Arg	Ala	Arg	Gln	Ala	Phe	
157					485					490					495		
159	cgc	atc	aag	ggt	gcc	gcg	tca	cgg	cag	aac	tca	gaa	gaa	gca	agc	ctc	1536
160	Arg	Ile	Lys	Gly	Ala	Ala	Ser	Arg	Gln	Asn	Ser	Glu	Glu	Ala	Ser	Leu	
161				500					505					510			
163	ccc	gga	gag	gac	att	gtg	gat	gac	aag	agc	tgc	ccc	tgc	gag	ttt	gtg	1584
164	Pro	Gly	Glu	Asp	Ile	Val	Asp	Asp	Lys	Ser	Cys	Pro	Cys	Glu	Phe	Val	
165			515					520						525			
167	acc	gag	gac	ctg	acc	ccg	ggc	ctc	aaa	gtc	agc	atc	aga	gcc	gtg	tgt	1632
168	Thr	Glu	Asp	Leu	Thr	Pro	Gly	Leu	Lys	Val	Ser	Ile	Arg	Ala	Val	Cys	
169		530					535					540					
171	gtc	atg	cgg	ttc	ctg	gtg	tcc	aag	cgg	aag	ttc	aag	gag	agc	ctg	cgg	1680
172	Val	Met	Arg	Phe	Leu	Val	Ser	Lys	Arg	Lys	Phe	Lys	Glu	Ser	Leu	Arg	
173	545					550					555					560	
175	ccc	tac	gac	gtg	atg	gac	gtc	atc	gag	cag	tac	tca	gcc	ggc	cac	ctg	1728
176	Pro	Tyr	Asp	Val	Met	Asp	Val	Ile	Glu	Gln	Tyr	Ser	Ala	Gly	His	Leu	
177					565					570					575		
179	gac	atg	ctg	tcc	cga	att	aag	agc	ctg	cag	tcc	agg	caa	gag	ccc	cgc	1776
180	Asp	Met	Leu	Ser	Arg	Ile	Lys	Ser	Leu	Gln	Ser	Arg	Gln	Glu	Pro	Arg	
181				580					585					590			
183	ctg	cct	gtc	cag	cag	ggg	aca	aga	acg	ggg	tgg	gct	tct	ggg	aca	aag	1824
184	Leu	Pro	Val	Gln	Gln	Gly	Thr	Arg	Thr	Gly	Trp	Ala	Ser	Gly	Thr	Lys	
185			595				600							605			
187	ccc	act	gtg	gcc	cat	ggt	ggg	agt	gca	ggg	ggt	gtg	tgg	gcg	ggg	cct	1872
188	Pro	Thr	Val	Ala	His	Gly	Gly	Ser	Ala	Gly	Gly	Val	Trp	Ala	Gly	Pro	
189		610					615							620			
191	cct	ccc	cac	cca	cgt	cgg	cct	ctg	tca	gct	tct	ggt	gtg	tct	tca	caa	1920

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192 Pro Pro His Pro Arg Arg Pro Leu Ser Ala Ser Val Val Ser Ser Gln
193 625                630                635                640
195 agt ctg ttt taa
196 Ser Leu Phe
200 <210> SEQ ID NO: 2
201 <211> LENGTH: 643
202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 2
207 Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
208 1                5                10                15
211 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
212                20                25                30
215 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
216                35                40                45
219 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
220                50                55                60
223 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
224 65                70                75                80
227 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
228                85                90                95
231 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
232                100               105               110
235 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
236                115               120               125
239 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
240                130               135               140
243 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
244 145                150               155               160
247 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
248                165               170               175
251 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
252                180               185               190
255 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
256                195               200               205
259 Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
260                210               215               220
263 Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
264 225                230               235               240
267 Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
268                245               250               255
271 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
272                260               265               270
275 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
276                275               280               285
279 Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
280                290               295               300
283 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
284 305                310               315               320

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```

287 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
288           325           330           335
291 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
292           340           345           350
295 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
296           355           360           365
299 Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
300           370           375           380
303 Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
304 385           390           395           400
307 Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser
308           405           410           415
311 Lys Gly Ser Pro Cys Arg Gly Pro Leu Cys Gly Cys Cys Pro Gly Arg
312           420           425           430
315 Ser Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg
316           435           440           445
319 Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg
320           450           455           460
323 Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val
324 465           470           475           480
327 Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe
328           485           490           495
331 Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu
332           500           505           510
335 Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val
336           515           520           525
339 Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys
340           530           535           540
343 Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg
344 545           550           555           560
347 Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
348           565           570           575
351 Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Gln Glu Pro Arg
352           580           585           590
355 Leu Pro Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys
356           595           600           605
359 Pro Thr Val Ala His Gly Gly Ser Ala Gly Gly Val Trp Ala Gly Pro
360           610           615           620
363 Pro Pro His Pro Arg Arg Pro Leu Ser Ala Ser Val Val Ser Ser Gln
364 625           630           635           640
367 Ser Leu Phe
371 <210> SEQ ID NO: 3
372 <211> LENGTH: 1878
373 <212> TYPE: DNA
374 <213> ORGANISM: Homo sapiens
376 <220> FEATURE:
377 <221> NAME/KEY: CDS
378 <222> LOCATION: (1)..(1878)
380 <400> SEQUENCE: 3

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RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : F:\G-194US04PCT-Subst-Seq-List.txt

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:37; N Pos. 10,5363,8080,10296,14528,15336,15457,16288,16306,16307
Seq#:37; N Pos. 16316,16397,56012,57662
Seq#:37; N Pos. 60402,61110,98207,98208,98209,98210,98211,99743,108055
Seq#:37; N Pos. 109094,109125
Seq#:37; N Pos. 118900,119024,119025,119026,119027,119028,119029,119030
Seq#:37; N Pos. 119031,119032,119033,119034,119035,119036,119037,119038
Seq#:37; N Pos. 119039,119040,119041,119042,119043,119044,119045,119046
Seq#:37; N Pos. 119047,119048,119049,119050,119051,119052,119053,119054
Seq#:37; N Pos. 119055,119056,119057,119058,119059,119060,119061,119062
Seq#:37; N Pos. 119063,119064,119065,119066,119067,119068,119069,119070
Seq#:37; N Pos. 119071,119072,119073,119074,119075,119076,119077,119078
Seq#:37; N Pos. 119079,119080,119081,119082,119083,119084,119085,119086
Seq#:37; N Pos. 119087,119088,119089,119090,119091,119092,119093,119094
Seq#:37; N Pos. 119095,119096,119097,119098,119099,119100,119101,119102
Seq#:37; N Pos. 119103,119104,119105,119106,119107,119108,119109,119110
Seq#:37; N Pos. 119111,119112,119115,119116,119117,119118,119119,119120
Seq#:37; N Pos. 119121,119123,141674,142063,142137,142967,143077,143506
Seq#:37; N Pos. 143587,143629,149079

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32
Seq#:33,34,35,36,39,40,41,42,43,44,45,46,47

VERIFICATION SUMMARY

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Input Set : F:\G-194US04PCT-Subst-Seq-List.txt

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L:1938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:2122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:5314
L:2214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:8074
L:2288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:10294
L:2428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:14494
L:2456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:15334
L:2460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:15454
L:2486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16234
L:2488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16294
L:2490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16354
L:3810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:55954
L:3866 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:57634
L:3958 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:60394
L:3980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:61054
L:5244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:98202
L:5304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:99719
L:5584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:108053
L:5618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:109073
L:5944 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:118853
L:5948 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:118973
L:5950 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:119033
L:5952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:119093
L:6726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:141615
L:6740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:142035
L:6742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:142095
L:6770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:142935
L:6774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143055
L:6788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143475
L:6790 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143535
L:6792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143595
L:6980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:149027